

05081147CRF  
SEQUENCE LISTING

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<120> PROTEIN CRYSTAL COMPRISING THE PROCESSIVITY CLAMP FACTOR  
OF DNA POLYMERASE AND A LIGAND, AND ITS USES

<130> 0508-1147

<140> US 10/561,867  
<141> 2006-07-06

<150> PCT/EP2004/006942  
<151> 2004-06-25

<150> EP 03291596.9  
<151> 2003-06-27

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<170> PatentIn version 3.5

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Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp		
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Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu		
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Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg		
65 70 75 80		
Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg		
85 90 95		
Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro		
100 105 110		
Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe		
115 120 125		
Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe		
130 135 140		
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe		

145

150

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155

160

Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg  
165 170 175

Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser  
180 185 190

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp  
195 200 205

Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg  
210 215 220

Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg  
225 230 235 240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu  
245 250 255

Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile  
260 265 270

Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn  
275 280 285

Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu  
290 295 300

Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn  
305 310 315 320

Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val  
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Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu  
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<213> Artificial Sequence

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Arg Gln Leu Val Leu Gly Leu  
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&lt;213&gt; Artificial Sequence

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E. coli DNA polymerase III

&lt;400&gt; 7

Leu Asn Gly Met Leu Phe Glu Thr Glu Gly Glu Glu Leu Arg Thr Val  
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20 25 30Ser Leu Pro Ser His Ser Val Ile Val Pro Arg Lys Gly Val Ile Glu  
35 40 45Leu Met Arg Met Leu Asp Gly Gly Asp Asn Pro Leu Arg Val Gln Ile  
50 55 60Gly Ser Asn Asn Ile Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser  
65 70 75 80Lys Leu Val Asp Gly Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys  
85 90 95Asn Pro Asp Lys His Leu Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala  
100 105 110Phe Ala Arg Ala Ala Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg  
115 120 125Leu Tyr Val Ser Glu Asn Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu  
130 135 140Gln Glu Glu Ala Glu Glu Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu  
145 150 155 160Met Glu Ile Gly Phe Asn Val Ser Tyr Val Leu Asp Val Leu Asn Ala  
165 170 175Leu Lys Cys Glu Asn Val Arg Met Met Leu Thr Asp Ser Val Ser Ser  
180 185 190

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Val Gln Ile Glu Asp Ala Ala Ser Gln Ser Ala Ala Tyr Val Val Met  
195 200 205

Pro Met  
210